

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 08:24:57 ; Search time 76.45 Seconds

(without alignments)
196,868 Million cell updates/sec

Title: US-09-351-778A-10

Sequence: 1 MGSRTAPRTDYRMTATGL.....RPPIRPIGLKPCSLLOYD 87

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriaph:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	79.3	101	12	091023 human adeno
2	53	60.9	101	12	091236 human adeno
3	18	20.7	94	12	012392 human adeno
4	7	8.0	83	12	088422 spiroplasma
5	7	8.0	85	11	03WV20 retus norv
6	7	8.0	87	10	094H62 oryza sativ
7	7	8.0	160	16	098268 rhizobium j
8	7	8.0	197	16	092XL7 chlamydia m
9	7	8.0	197	16	09JSG7 chlamydia p
10	7	8.0	228	2	09RBX8 pseudomonas
11	7	8.0	245	8	09R3V9 nephroselini
12	7	8.0	316	10	09C9Z6 arabidopsis
13	7	8.0	387	16	099X15 staphylococ
14	7	8.0	391	16	097GC3 clostridium
15	7	8.0	392	10	09AX94 oryza sativ
16	7	8.0	404	5	09VIM7 drosophila

17	7	8.0	490	10	09FSS8	09fs8 oryza sativ
18	7	8.0	536	5	045994	045994 caenorhabdi
19	7	8.0	604	5	09VQ31	09vq31 drosophila
20	7	8.0	635	5	09VJT7	09vj7 drosophila
21	7	8.0	649	5	09WKD0	09wk0 drosophila
22	7	8.0	965	2	032494	032494 bacteroides
23	7	8.0	1175	16	091356	091356 pseudomonas
24	7	8.0	2689	5	095Y78	095y78 leishmania
25	6	6.9	26	4	09BUB3	09bud3 homo sapien
26	6	6.9	53	13	09YH36	09yh36 coturnix co
27	6	6.9	64	2	09F347	09f347 streptomyces
28	6	6.9	69	13	09DEC6	09dec6 gallus gall
29	6	6.9	73	15	087603	087603 chimpanzee
30	6	6.9	76	4	09CEM4	09cem4 homo sapien
31	6	6.9	77	12	064868	064868 avian adeno
32	6	6.9	82	16	09PCC9	09pc9 xyella fas
33	6	6.9	83	16	09PE04	09pe4 xyella fas
34	6	6.9	89	10	094J51	094j51 oryza sativ
35	6	6.9	89	16	09AA87	09aa87 caulobacter
36	6	6.9	91	4	09H4V4	09h4v4 homo sapien
37	6	6.9	94	16	09PCB2	09pcb2 xyella fas
38	6	6.9	94	16	09PCA5	09pcas xyella fas
39	6	6.9	95	11	09OZG8	09ozg8 rattus norv
40	6	6.9	97	3	0977L9	0977l9 schistosach
41	6	6.9	110	17	097A58	097a58 thermoplasma
42	6	6.9	113	16	09K1B1	09k1b1 neisseria m
43	6	6.9	113	16	09JX91	09jx91 neisseria m
44	6	6.9	115	2	09KXU2	09kxu2 streptomyces
45	6	6.9	115	3	09P8V1	09p8v1 ashbya goss

ALIGNMENTS

RESULT 1
ID Q91023 PRELIMINARY; PRT; 101 AA.
AC Q91023;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 11.6K PROTEIN.
OS Human adenovirus type 2.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=105;
RA Borchering F., Piling-Akerblom P.;
RT "Adenoviruses of subgenus C with different organ tropism."
DR EMBL; AJ293915; CAC67721.1; -
SQ SEQUENCE 101 AA; 11662 MW; 914F50AC2F8B284F CRC64;

Query Match 79.3%; Score 69; DB 12; Length 101;
Best Local Similarity 100.0%; Pred. No. 2e-66;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 APTTDYRMTATGTSALNPOVHAFAVDNADSLDMWFSIALMFVCLITIMLICCKRRR 66
DB 7 APTTDYRMTATGTSALNPOVHAFAVDNADSLDMWFSIALMFVCLITIMLICCKRRR 66
QY 67 ARPPIYRPI 75
DB 67 ARPPIYRPI 75
RESULT 2
Q91206 PRELIMINARY; PRT; 101 AA.
AC Q91206;
DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE 11.6K PROTEIN.
 OS Human adenovirus type 2.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=10515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PRET.
 RA Borchering F., Pring-Akerdrom P.;
 RT "Adenoviruses of subgenus C with different organ tropism";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A7293913; CAC67704.1; -
 SO SEQUENCE 101 AA; 11704 MW; E13857DC5891E85B CRC64;

Query Match 60.9%; Score 53; DB 12; Length 101;
 Best Local Similarity 100.0%; Pred. No. 3; 3e-49;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 ALNLPQVHAFVNDMSLDMWFSLMFVCLIIIMLICCKRRRAPPYRPI 75
 DB 23 ALNLPQVHAFVNDMSLDMWFSLMFVCLIIIMLICCKRRRAPPYRPI 75

RESULT 3
 ID 012392 PRELIMINARY; PRT; 94 AA.
 AC 012392;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-JAN-1998 (Tremblrel. 05, Last annotation update)
 DE 11.6K PROTEIN.
 GN AD1/E3-11.6K.
 OS Human adenovirus type 1.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=10533;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HANNOVER / ADRIAN;
 RA Reichmann H., Scharschmidt E., Gelsler B., Hausmann J., Ortmann D.,
 BAUER U., Flunker G., Seidel W.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y11257; CAA72127.1; -
 FT NON-TER 94
 SO SEQUENCE 94 AA; 10674 MW; D148B5AF771862 CRC64;

Query Match 20.7%; Score 18; DB 12; Length 94;
 Best Local Similarity 100.0%; Pred. No. 1; 4e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 MMWFSLMFVCLIIIMWL 58
 DB 35 MMWFSLMFVCLIIIMWL 52

RESULT 4
 ID 088422 PRELIMINARY; PRT; 83 AA.
 AC 088422;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE SPV1-C74, COMPLETE GENOME.
 OS Spiroplasma virus.
 OC Viruses; unclassified viruses.
 OX NCBI_TaxID=12338;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPV1-C74;
 RA Bebear C.M., Aulio P., Bove J., Renaudin J.;
 RT "Spiroplasma citri virus SPV1. Characterization of viral sequences

RT present in the spiroplasma host chromosome.";
 RL Curr. Microbiol. 32:1-7(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPV1-C74;
 RA Renaudin J.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U28974; AAA85015.1; -
 SO SEQUENCE 83 AA; 9398 MW; D4969373802BFFA8 CRC64;

Query Match 8.0%; Score 7; DB 12; Length 83;
 Best Local Similarity 100.0%; Pred. No. 8; 5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 TGLTSAL 24
 DB 30 TGLTSAL 36

RESULT 5
 ID 09WV20 PRELIMINARY; PRT; 85 AA.
 AC 09WV20;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE PROTEIN TYROSINE PHOSPHATASE EPSILON (FRAGMENT).
 GN PREPESILON.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9915422; PubMed=9914474;
 RA Tanuma N., Nakamura K., Kikuchi K.;
 RT "Distinct promoters control transmembrane and cytosolic protein
 tyrosine phosphatase epsilon expression during macrophage
 differentiation";
 RL Eur. J. Biochem. 259:46-54(1999).
 DR EMBL: D89173; BAA78711.1; -
 FT NON-TER 85
 FT NON-TER 85
 SO SEQUENCE 85 AA; 9031 MW; CFFD2DABE70A02523 CRC64;

Query Match 8.0%; Score 7; DB 11; Length 85;
 Best Local Similarity 100.0%; Pred. No. 8; 6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 PCSLLDQ 85
 DB 25 PCSLLDQ 31

RESULT 6
 ID 094H62 PRELIMINARY; PRT; 87 AA.
 AC 094H62;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOHETICAL 9.9 KDA PROTEIN.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eurythaleae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Bell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,

RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Taitlin T.,
 RA Riggs F., Hsiao J., Zisman V., Blunt S., Pal G., Vanaken S.E.,
 RA Uterback T.R., Feldblum T.V., Quackenbush J., Salzberg S.L.,
 RA White O., Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSJNB0057P11 genomic sequence."
 BL Submitted (MUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC084767; AKK72273.1; -;
 KW Hypothetical protein.
 SO SEQUENCE 87 AA; 9941 MW; 092E2A6E9D0A42CE CRC64;

Query Match 8.0%; Score 7; DB 10; Length 87;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 LKRRAR 68
 DB 48 LKRRAR 54

RESULT 7
 ID 0982G8 PRELIMINARY; PRT; 160 AA.
 AC 0982G8;
 DT 01-OCT-2001 (TReMBLrel. 18, Created)
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
 DE MLR9079 PROTEIN.
 GN MLR9079.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Plasmid pML.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 CX NCBI_Taxid=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAF303099;
 RC MEDLINE=21082930; PubMed-11214968;
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Matsumoto A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti."
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP003015; BAB54491.1; -;
 KM Plasmid; Complete proteome.
 SQ SEQUENCE 160 AA; 17696 MW; 85A9C5A9233D9A50 CRC64;

Query Match 8.0%; Score 7; DB 16; Length 160;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSTIAP 8
 DB 28 TGSTIAP 34

RESULT 8
 ID 092XL7 PRELIMINARY; PRT; 160 AA.
 AC 092XL7;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DE HYPOTHEICAL PROTEIN SMA2279.
 GN SMA2279.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plasmid pSymb (megaplasmid I).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.

OX NCBI_Taxid=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396509; PubMed-11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Bartlett-Huddle F., Bowser L., Capela D., Galibert F., Guzy J.,
 RA Gujral M., Hong A., Huizer L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kahan S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 RT Sinorhizobium meliloti pSymb megaplasmid."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 DR EMBL: AE007307; AAK65885.1; -;
 KW Hypothetical protein; Plasmid; Complete proteome.
 SQ SEQUENCE 160 AA; 17966 MW; 98B84EBE18A1B34 CRC64;

Query Match 8.0%; Score 7; DB 16; Length 160;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSTIAP 8
 DB 28 TGSTIAP 34

RESULT 9
 ID 09JSG7 PRELIMINARY; PRT; 197 AA.
 AC 09JSG7;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 GN CT142 HYPOTHEICAL PROTEIN_2.
 GN CPJ0259.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_Taxid=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RC MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA."
 RL Nucleic Acids Res. 28:2311-2314(2000).
 DR EMBL: AP002545; BAA98469.1; -;
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR InterPro: IPR000531; TonB_boxC.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 SQ SEQUENCE 197 AA; 22016 MW; EAA69A27851F790D CRC64;

Query Match 8.0%; Score 7; DB 16; Length 197;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
 DB 74 ATGLTSA 80

RESULT 10
 ID 09RBX8 PRELIMINARY; PRT; 228 AA.
 AC 09RBX8;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DE HYPOTHEICAL 24.1 KDA PROTEIN.

OS Pseudomonas indologera.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Vogesella.
 NCBI_TaxID=45465;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC19706;
 RA van de Loo F.J., Keese P., Llewellyn D.;
 RT Structural and regulatory genes controlling indigoidine production in
 RT Vogesella indologera: involvement of a peptide synthetase homolog.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TETR/ACNR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC EMBL: AF088856; AAD54003.1;
 DR InterPro: IPR001647; HTR_Petr.
 DR Pfam: PF00440; tetr.1.
 DR PRINTS: PRO0455; HTRHTR.
 KW DNA-binding; Hypothetical protein; Transcription regulation.
 SO SEQUENCE 228 AA; 2410 MW; A928DE1AF040659B CRC64;

Query Match 8.0%; Score 7; DB 2; Length 228;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRAPP 70
 DB 23 RRRAPP 29

RESULT 11
 09T3Y9 PRELIMINARY; PRT; 245 AA.

AC 09T3Y9;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE HYPOTHEICAL 27.2 KDA PROTEIN.
 OS Nephroselmis olivacea.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
 OC Chlorodendroales; Chlorodendraceae; Nephroselmis.
 NCBI_TaxID=31312;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-9938694; PubMed-10468594;
 RA Turmel M., Ollis C., Lemieux C.;
 RT The complete chloroplast DNA sequence of the green alga Nephroselmis
 RT olivacea: Insights into the architecture of ancestral chloroplast
 RT genomes.;
 RT Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Turmel M., Ollis C., Lemieux C.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF137379; AAD54818.1;
 DR EMBL: AF137379; AAD54871.1;
 KW Hypothetical protein; Chloroplast.
 SO SEQUENCE 245 AA; 27217 MW; 74FDF5F5F229F7 CRC64;

Query Match 8.0%; Score 7; DB 8; Length 245;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 TGLTSL 24
 DB 204 TGLTSL 210

RESULT 12
 09C9Z6 PRELIMINARY; PRT; 316 AA.
 AC 09C9Z6;

DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE HYPOTHEICAL 34.7 KDA PROTEIN (AT350860/F17014_7).
 GN F17014.7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA.
 RX MEDLINE-21016720; PubMed-11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansong W., Unsel M.,
 RA Farman B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Delseny M., Boutry M., Grivell L.A., Mache R., Pulgomech P.,
 RA De Simone V., Choisme N., Artiguenave F., Robert C., Brotier P.,
 RA Mincker P., Cattolico L., Weissbach J., Saurin W., Queller F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wumbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
 RA Wedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppe S., Simonelli B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.H., Nordstiek G.,
 RA Reichelt J., Scharfe M., Schuen O., Bargues M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
 RA Cooke R., Landie M., Berger-Liauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.P., Cottet A., Casacuberta E.,
 RA Monfort A., Argitrou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haese D., Schoof H., Ruid S., Zaccaria P., Hoes H.-M.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii S., Shea T.P.,
 RA Creasy T.H., Haas B., Malters P., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Miltischer J., Sellers P., Gill J.E., Feldlyan T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Aamizu Y.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida A.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Nakane A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana.";
 RT Nature 408:820-822(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 RA Bower L., Carlini P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamuya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis ORF clones.";
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 RA Bower L., Carlini P., Dale J.M., Gibson H.A., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamuya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones.";
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC012362; AAG51364.1;
 DR EMBL: AY050687; AAL06875.1;
 DR EMBL: AY045678; AAK74036.1;
 KW Hypothetical protein.
 SO SEQUENCE 316 AA; 34732 MW; 5B54FCCF59A5B85B CRC64;

Query Match 8.0%; Score 7; DB 10; Length 316;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 LNSALNPQ 28
 |||||
 DB 146 SALNLPQ 152

RESULT 13

O99X15 PRELIMINARY; PRT: 387 AA.

AC O99X15;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE SA0200 PROTEIN (HYPOTHETICAL PROTEIN SAV0207).
 GN SA0200 OR SAV0207.
 OS Staphylococcus aureus (strain N315), and
 OC Staphylococcus aureus (strain Mu50).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_Taxid=158879, 158878;
 RN [1]
 RP SEQUENCE FROM N.A.

RC SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
 RC MEDLINE=21311952; PubMed=1418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Imai T., Ito T.,
 RA Kanamori M., Matsunari H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mitani-Uti Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RT Lancet 357:1225-1240(2001).
 DR EMBL: AP003129; BAB41422.1;
 DR EMBL: AP003358; BAB56369.1;
 DR InterPro: IPR000515; BPD.transp.
 DR Pfam: PF00528; BPD.transp.1.
 KW Complete proteome: Hypothetical protein
 SQ SEQUENCE 387 AA; 43077 MW; 08f9fb4bca6dc8 CRC64;

Query Match 8.0%; Score 7; DB 16; Length 387;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 LNSALNL 26
 |||||
 DB 27 LNSALNL 33

RESULT 14

O97GC3 PRELIMINARY; PRT: 391 AA.

AC O97GC3;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE AICAR TRANSFORMYLASE DOMAIN OF PURH-LIKE PROTEIN.
 GN CAC2445.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium
 OX NCBI_Taxid=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RC MEDLINE=21359325; PubMed=1466286;
 RX Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,

RA Gibson R., Lee H.M., Dubois J., Qiu D., Hattl J., Wolf Y.I.,
 RA Tatusov R.L., Sabate F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum."
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AE007744; AAK80399.1;
 DR InterPro: IPR002695; AICARFT_IMPCHas.
 DR Pfam: PF01808; AICARFT_IMPCHas; 1.
 DR ProDom: PD004666; AICARFT_IMPCHas; 1.
 KW Complete proteome.
 SQ SEQUENCE 391 AA; 43547 MW; 18642c6ba97e909e CRC64;

Query Match 8.0%; Score 7; DB 16; Length 391;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
 |||||
 DB 58 ATGLTSA 64

RESULT 15

O9AX94 PRELIMINARY; PRT: 392 AA.

AC O9AX94;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE P0501G01.23 PROTEIN.
 GN P0501G01.23
 OS Oryza sativa (rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzae; Oryza.
 OX NCBI_Taxid=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0501G01."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP002819; BAB21094.1;
 SQ SEQUENCE 392 AA; 40501 MW; BB4f44827a7EDC34 CRC64;

Query Match 8.0%; Score 7; DB 10; Length 392;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRARPP 70
 |||||
 DB 133 RRRARPP 139

Search completed: June 21, 2002, 08:24:57
 Job time: 282 sec
